

SEQUENCE LISTING

<110> Ecole Polytechnique Fédérale de Lausanne (EPFL)

<120> Method for identification of suitable fragmentation sites in a reporter protein

<130> PEPF001WO

<150> US 34,404 JM-213

<151> 2003-10-09

<160> 66

<170> PatentIn version 3.1

<210> 1

<211> 672

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> modified_base

<222> (186)..(186)

<223> silent point mutation introduced to generate HindIII restriction site

<300>

<308> NCBI / NC_001136

<309> 2004-08-30

<400> 1

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atgtctgttta ttaatttcac aggtagttct ggtccattgg tgaagatttg cggcttgacag      60
agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt      120
gtgcccataa gaaagagaac aattgaccgg gttattgcaa ggaatttc aagtcttgta      180
aaagcatata aaaatagttc aggcactccg aaatacttgg ttggcgtgtt togtaataca      240
cctaaggagg atgttttggc tctgggtcaat gattacggca ttgatatcgt ccaactgcac      300
ggagatgagt cgtggcaaga ataccaagag ttcctcgggt tgccagtatt taaagactc      360
gtattttcaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt      420
attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttgattg gaactcgatt      480
tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctgggtgga      540
ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttatagg tgttgatgta      600
agcggagggtg tggagacaaa tgggtgtaaaa gactctaaca aaatagcaaa tttcgtcaaa      660
aatgctaaga aa                                         672

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<210> 2

<211> 224

<212> PRT

<213> *Saccharomyces cerevisiae*

<300>

<308> NCBI / NC_001136

<309> 2004-08-30

<400> 2

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Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1           5           10          15

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```

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
          20          25          30

```

```

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
          35          40          45

```

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Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
          50          55          60

```

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly
195 200 205

Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
210 215 220

<210> 3

<211> 132

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> modified_base

<222> (22)..(22)

<223> point mutation

<400> 3

atgtctgttta ttaatttcac atgtagttct ggtccatttg tgaaagtttg cggcttgacag 60
 agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120
 gtgccaata ga 132

<210> 4

<211> 44

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 4

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val
 1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
 20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg
 35 40

<210> 5

<211> 540

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 5
 aagagaacaa ttgacccggt tattgcaagg aaaatttcaa gtcttgtaaa agcatataaa 60
 aatagttcag gcaactccgaa atacttggtt ggcgtgtttc gtaatcaacc taaggaggat 120
 gttttggctc tgggtcaatga ttaaggcatt gatatogtcc aactgcacgg agatgagtcg 180
 tggcaagaat accaagagtt octcggtttg ccagttatta aaagactcgt atttccaaaa 240
 gactgcaaca tactactcag tgcagcttca cagaaacctc attcgtttat tcccttgttt 300
 gattcagaag cagggtgggac aggtgaactt ttggattgga actcgatttc tgactgggtt 360
 ggaaggcaag agagccccga gagcttacat tttatgtag ctggtggact gacgccagaa 420
 aatgttggtg atgcgcttag attaaatggc gttattggtg ttgatgtaag cggaggtgtg 480
 gagacaaatg gtgtaaaaga ctctaacaaa atagcaaatt tcgtcaaaaa tgctaagaaa 540

<210> 6

<211> 180

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 6

Lys Arg Thr Ile Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val
1 5 10 15

Lys Ala Tyr Lys Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val
20 25 30

Phe Arg Asn Gln Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr
35 40 45

Gly Ile Asp Ile Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr
50 55 60

Gln Glu Phe Leu Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys
65 70 75 80

Asp Cys Asn Ile Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe
85 90 95

Ile Pro Leu Phe Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp
100 105 110

Trp Asn Ser Ile Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser
115 120 125

Leu His Phe Met Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp
130 135 140

Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
145 150 155 160

Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys
165 170 175

Asn Ala Lys Lys
180

<210> 7

<211> 159

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 7

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atgtctgttta ttaatttcac aggtagttct ggtccattgg tgaaagtttg cggcttgacag      60
agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt      120
gtgccaataa gaaagagaac aattgaccgg gttattgca                                159

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<210> 8

<211> 53

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 8

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Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1           5           10          15

```

```

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
      20           25           30

```

```

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
      35           40           45

```

```

Asp Pro Val Ile Ala
      50

```

<210> 9

<211> 516

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 9

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gcaaggaaaaa tttaagtct tgtaaaagct tataaaaata gttcaggcac tccgaaatac      60
ttggttggcg tgtttcgtaa tcaacctaa gaggatgttt tggtctcgtt caatgattac      120

```

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ggcattgata tcgtccaact gcaacggagat gagtcgtggc aagaatacca agagtctctc 180
ggtttgcag ttattaaaag actcgtattt ccaaaaagact gcaacatact actcagtgc 240
gcttcacaga aacctcattc gtttattccc ttgtttgatt cagaagcagg tgggacaggt 300
gaacttttgg attggaactc gatttctgac tgggttgga ggcaagagag ccccgagagc 360
ttacatttta tgtagctgg tggactgacg ccagaaaaatg ttggtgatgc gcttagatta 420
aatggcgtta ttggtgttga tgtaagcgga ggtgtggaga caaatggtgt aaaagactct 480
aacaaaatag caaatctcgt caaaaatgct aagaaa 516

```

<210> 10

<211> 172

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 10

```

Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys Asn Ser Ser Gly
1             5             10             15

```

```

Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln Pro Lys Glu Asp
                20             25             30

```

```

Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile Val Gln Leu His
35             40             45

```

```

Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu Gly Leu Pro Val
50             55             60

```

```

Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile Leu Leu Ser Ala
65             70             75             80

```

```

Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe Asp Ser Glu Ala
85             90             95

```

```

Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile Ser Asp Trp Val
100            105            110

```

```

Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met Leu Ala Gly Gly
115            120            125

```

```

Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu Asn Gly Val Ile
130            135            140

```

Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly Val Lys Asp Ser
 145 150 155 160

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
 165 170

<210> 11

<211> 561

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 11
 atgtotgttta ttaatttcac aggtagttct ggtccattgg tgaagtttg oggottgcag 60
 agcacagagg cgcgagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120
 gtgcccataa gaaagagaac aattgaccog gttattgcaa ggaaaatttc aagtcttgta 180
 aaagcttata aaaatagttc aggcactocg aaataacttg ttggcgtgtt togtaatcaa 240
 cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac 300
 ggagatgagt cgtggcaaga ataccaagag ttctctcggt ttgcagttat taaaagactc 360
 gtattttcaa aagactgcaa catactactc agtgacgctt cacagaaacc tcattcggtt 420
 attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt 480
 tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga 540
 ctgacgccag aaaatgttgg t 561

<210> 12

<211> 187

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 12

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
 1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
 20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
 35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
 50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
 65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
 85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
 100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
 115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
 130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
 145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
 165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly
 180 185

<210> 13

<211> 111

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 13
 gatgcgctta gattaaatgg cgttattggt gttgatgtaa gcggaggtgt ggagacaaat 60
 ggtgtaaaag actctaacaa aatagcaaat ttcgtcaaaa atgctaagaa a 111

<210> 14

<211> 37

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 14

Asp	Ala	Leu	Arg	Leu	Asn	Gly	Val	Ile	Gly	Val	Asp	Val	Ser	Gly	Gly
1				5					10					15	

Val	Glu	Thr	Asn	Gly	Val	Lys	Asp	Ser	Asn	Lys	Ile	Ala	Asn	Phe	Val
			20					25						30	

Lys	Asn	Ala	Lys	Lys
			35	

<210> 15

<211> 612

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> mutation

<222> (22)..(22)

<223> point mutation

<220>

<221> deletion

<222> (612)..(612)

<223> missing sequence after base 612 of wild-type: GAGACAAATGGTGTAAGAAG
ACTCT

<400> 15															
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agcaca	gagg	cgcaga	atg	tgctct	agat	tcgatg	ctg	acttgct	ggg	tattata	tatgt			120	
gtgccc	aata	gaaaga	gaac	aattgac	ccg	gttatt	gcaa	ggaaaa	atttc	aagtct	tgt			180	
aaagct	tata	aaaata	ggtc	aggcact	ccg	aaatact	tgg	ttggcgt	gtt	togta	atcaa			240	

```

cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac    300
ggagatgagt cgtggcaaga ataccaagag ttctctcggtt tgccagttat taaaagactc    360
gtattttcaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcggtt    420
attcccttgt ttgattcaga agcagggtggg acagggtgaac ttttggattg gaactcgatt    480
tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga    540
ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttatttg tgttgatgta    600
agcggaggtg tg                                                    612

```

<210> 16

<211> 204

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 16

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Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val
1              5              10              15

```

```

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
                20              25              30

```

```

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
35              40              45

```

```

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
50              55              60

```

```

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65              70              75              80

```

```

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
85              90              95

```

```

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
100              105              110

```

```

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
115              120              125

```

```

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
130              135              140

```

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
 145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
 165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
 180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
 195 200

<210> 17

<211> 36

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> mutation

<222> (1)..(1)

<223> missing sequence before base 1 of SEQ17, corresponding to base 63
 7 of wild-type: GAGACAAATGGTGTAAAAGACTCT

<400> 17
 aacaaaatag caaatctgct caaaaatgct aagaaa

36

<210> 18

<211> 12

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 18

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
 1 5 10

<210> 19

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> first of a pair of peptides (together with peptide C2), that associate into an anti-parallel coiled coil (Biochemistry 37 (1998), 12603-12610)

<400> 19

Met	Asp	Tyr	Lys	Asp	Glu	Ser	Gly	Gln	Ala	Leu	Glu	Lys	Glu	Leu	Ala
1				5					10					15	

Gln	Asn	Glu	Trp	Glu	Leu	Gln	Ala	Leu	Glu	Lys	Glu	Leu	Ala	Gln	Leu
		20					25						30		

Glu	Lys	Glu	Leu	Gln	Ala	Gly	Ser	Gly	Ser	Gly
		35						40		

<210> 20

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> second of a pair of peptides (together with peptide C1), that associate into an anti-parallel coiled coil (Biochemistry 37 (1998), 12603-12610)

<400> 20

Gly	Gly	Ser	Gly	Ser	Gly	Gln	Ala	Leu	Lys	Lys	Lys	Leu	Ala	Gln	Leu
1				5					10					15	

Lys	Trp	Lys	Leu	Gln	Ala	Leu	Lys	Lys	Lys	Asn	Ala	Gln	Leu	Lys	Lys
			20					25					30		

Lys	Leu	Gln	Ala	Gly	Ser	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Ala
		35						40					45		

Phe	Leu
	50

<210> 21

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 21

cgatacgaat tcattggacaa ggattgtgaa atgaaacgc

39

<210> 22

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 22

aaaggaattg gcccaaatg agtgggagtt acaagcactt gagaa

45

<210> 23

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 23

ctcaatgttc gtgaactctt cctcgagcga gttgaactct tcttc

45

<210> 24

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 24

ctccttctca agttgagcga gctccttctc aagtgtttgt aactc

45

<210> 25

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 25

ggcacttaag aagaagttgg cgcagcttaa gtggaaactg ca

42

<210> 26

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 26

agctgggcat tcttcttctt aagagcttgc agtttccact taagct

46

<210> 27

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 27

aagaagaaga atgcccagct taagaagaag ctccaggctg gaagttac

48

<210> 28

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 28

atacgatggtt ccagattacg ctgcattttt ataagtcgac tggtc

45

<210> 29

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 29

gaccagtcga cttataaaaa tg

22

<210> 30

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for circular permutation of TRP1

<400> 30

gtaaaagctt ataaaaatag ttcag

25

<210> 31

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for circular permutation of TRP1

<400> 31

gaaatagcct aggatgtctg ttattaattt cacagg

36

<210> 32

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for circular permutation of TRP1

<400> 32

cagacatcct aggcattttc ttagcatttt tgacg

35

<210> 33

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for circular permutation of TRP1

<400> 33

tttataagct ttacaagac ttgaa

25

<210> 34

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 34

gtaacgaatt catggactac aa

22

<210> 35

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 35

catctttgggc caattccttt tccagtgcct gaccactttc gtctttgtag tccatgaatt

60

cgttac

66

<210> 36

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 36

caactctcttc ttaagtcgct gacctgatcc agatccaccg ttaacacctg aacctgatcc

60

ggcc

64

<210> 37

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 37

gtaatctgga acatcgtatg ggtaacttcc agcctggagc ttc 43

<210> 38

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for homologous recombination

<400> 38

gactctaaca aaatagcaaa ttctgtcaaa aatgctaaga aatagagggc cgcacatgt 60

aattag 66

<210> 39

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for homologous recombination

<400> 39

aactttcacc aatggaccag aactacctgt gaaattaata acagacattt tgagatccgg 60

gtttt 65

<210> 40

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 40

gcctgatcca gatccgcctt ctgggtgattc atcatottca

40

<210> 41

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 41

ggcggatctg gatcaggcaa gagaacaatt gacccggta

40

<210> 42

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 42

gcctgatcca gatccgccta taaaaggat tccgacacca

40

<210> 43

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ntrp fusions

<400> 43

gcctgatcca gatccgcctg caataaccgg gtcaattgt

39

<210> 44

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 44

ggcggatctg gatcaggcgc aaggaaaatt tcaagtcttg

40

<210> 45

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ntrp fusions

<400> 45

gcctgatcca gatccgccac caacattttc tggcgtcagt cc

42

<210> 46

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 46

ggcggatctg gatcaggcga tgcgcttaga ttaaatggc

39

<210> 47

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ntrp fusions

<400> 47

gcctgatcca gatccgccca cacctccgct tacatcaac

39

<210> 48

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 48

ggcggatctg gatcaggcaa caaaatag

28

<210> 49

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS315CUP1/ pRS316CUP1

<400> 49

agcaggatcc cattaccgac atttg

25

<210> 50

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS315CUP1/ pRS316CUP1

<400> 50
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